


```
US-09-417- 1716 agGagTCGAGAACCGA      gagCgTCgGcgGaggtgtgaagaagCTCTGCT
      | | | | | | | |
US-09-417- 1530 cAGtTCGAG  TCCGA      aagccGtAGTTCTGAaCCAAA      TCTGCTGA
      | | | | | | | |
US-09-417- 1596 AccaACcCcaacttctgtatgccaagggAGcTCCTGATCGCAAAgagccagagTAgTCA
      | | | | | | | |
consensus      -ag--TCgaagACCGatgatg----ggg-Agttctga-Gccaaag-ga-----tCTgGTga

US-09-417- 1766
US-09-417- 1576 TG
      | |
US-09-417- 1656 TcGgaagagatgaattatgagaggttaagtatataatttatttattgaactgtatcAGA
      | | | | | | | |
consensus      tgtgaagagtgaattatgagaggttaagtatataatttatttattgaactgtatcAGA

US-09-417- 1784 ctgtAAAGAGcCtcaaggttgatgtgtgtgagtgatcaagcgTcaAgttccatctca
      | | | | | | | |
US-09-417- 1587 gccCAAGAGc      agcACcactGaCGtAAagagtgAatTgt
      | | | | | | | |
US-09-417- 1717 cagatgtgacatgtgtactgagggagaaataccaAGctgtctctccctaGccaata
      | | | | | | | |
consensus      c-g-aaAgagC---g---ga-g-----a---a-c---g-cg-aa---t-ga--t-a

US-09-417- 1845 atAcAagTAgatcgatcgtTgtgtgAtgcagtgCaagtTgacctGagggagagcCAGcAG
      | | | | | | | |
US-09-417- 1626 gAAgactTttaaAtagTttctGAgttAttcCcatcttTATGcaactTttGcAGctG
      | | | | | | | |
US-09-417- 1778 aAaacaacGaggaGtGggggcaGagacAaAtgcGaggcAcATatgtATTactatAac
      | | | | | | | |
consensus      aAA-aa-tcga--a-tgttggg-aag--a--a-c-c---t--catg-g--tt--gcagcag

US-09-417- 1906 agAtgagTgtcttAcTgtctAGAGAGAggaatcGAATcaGcaactAAtcAAATaaatcaaa
      | | | | | | | |
US-09-417- 1687 ccGagATTTTAgACcAtatgAGAGa  ctAGAAAT  taAAgaaAAAT  gTtTt
      | | | | | | | |
US-09-417- 1839 tTAAATTTTAAcAcTgggcatTTa  gaa  ttTgggttgagACTT  caATaa
      | | | | | | | |
consensus      --A-attTta-Acc---t-gagagAgg-aagaat-----taa--AaATaa-t-taa

US-09-417- 1967 TTCCatlaaaaaaataaataaataaataaataaataaataaataaataaataaataa
      | | | | | | | |
US-09-417- 1738 TTCC      CttTtctTAggAAAAAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa
      | | | | | | | |
US-09-417- 1890 atTC      CccCTTaaTtTtTAAAAAaAaAaAaAaAaAaAaAaAaAaAaAaAa
      | | | | | | | |
consensus      tTCCatlaaaac---ttaaata-tAAAAAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa

US-09-417- 2028 aaaa
US-09-417- 1775
US-09-417- 1928 aactcgactagttc
consensus      aa--cgagactagttc

Alignment score = -1017.00
Scoring matrix:
```

```
4 |
5 |
8 |
-296
-396
```

4 5 8

> O <
0110 Intelligenetics
> O <

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 21 Nov 101 12:09:59- PST

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

4. US-09-417-251-8 (1-541)
8. US-09-417-251-16 (1-551)
5. US-09-417-251-10 (1-570)

Region Alignment: (listed in Clustered order)

US-09-417- 1 heepdaaagasaahnlhpfdfeggaedED fgdffsdf
US-09-417- 1 mriIvVL SLAT lllfslflllCDLl tddEdlgfIdpeSaapbhghy
US-09-417- 1 mgstmsppsfyVvlllllLlATlAaagSmdeevvDdLgylldnsddlptndpdpwpegd
consensus mgstmsppsfyVvlllLlATlAaagSmdeevvDdLgylldnsddlptndpdpwpegd

US-09-417- 38 ebsda DrdeYkAPEVDEKDVVVLKegNfAdfVeKnfVWVEFYAPWCGHCOALA
US-09-417- 48 hdddaIfgdfeepesYKQPEVDEKDVVVLKegNfAdfVeKnfVWVEFYAPWCGHCOALA
US-09-417- 62 yDDdDlIfgdqgdqdlIghQPEIdElthvVlaaaNfssFlaSShhVWVEFYAPWCGHCOALA
consensus -DdDa-----d---yKqPEVDEKDVVVLke-NfAdfV-snrfVWVEFYAPWCGHCOALA

US-09-417- 92 P EYAAATBELKGenVlAKVDATeENELsOKYDVQGFPTVYFFADGVHksYpGQR
US-09-417- 109 P EYAAATBELKGeVlLAKVDATeENELAQYDVQGFPTVHFFEDGJlHKpYNGQR
US-09-417- 123 pjsrrrrhLagstnpnpnfafALAKVDATeEdLlAQYDVQGFPTlIfFIdGvprYNGAR
consensus PglstrreyaaAaTeIkgenV-LAKVDATeENELaOKYDVQGFPTV-FF-DGvNh-YngQR

US-09-417- 147 TKDAIVTWlKKRIGPgiVNIstVEDaERlITsETKvVLGyLNSlVGPESuELAAASRLLED
US-09-417- 164 TKDAIVTWlGKRIGPgiVNIstVEDaORlITnETKvVLGfLNSlVGPESeELAAASRLLED
US-09-417- 184 TTeaIVdWlNKRIgPvqVNTsvdeAQsIlTgQdkaVlaFlDtlSGahSdELAAASRLLED
consensus TKDAIVTWl-KKIGPgiVn-TsvedAqrlIT-ekvVLGfLNSlVGPes-ELAAASRLLED

US-09-417- 208 VNFYQTVdVpVAKLFIeasakRPALVlLkKbaEKLnRFDGefSKsAlaEfVvANKLPLVT
US-09-417- 225 VNFYQTVdVpVAKLFIHDpVkrRPALlVlKKEEKLnHfGdGkFekSeIadFvFSnKLPVLT
consensus VNFYQTVdVpVAKLFIHDpVkrRPALlVlKKEEKLnHfGdGkFekSeIadFvFSnKLPVLT

US-09-417- 245 INFYQTSbDpVAKLFHIDaakRPsvVlLkKEEKlLfYDGeFkSaIagFvSANKLPLVT
consensus VNFYQTVdVpVAKLFHIda-akRPALVlLkKEEKLn-IDGef-kSaIa-fVvANKLPLVT

US-09-417- 269 kFTRESAPlIfEESIKKQlLlFAlSNDSEKlPIfEESkSKfPKGLIfVvEIdNEDVGKp
US-09-417- 286 lFTRESAPsvFEENRPKQlLlFAlSNDSEKlPIfEESkSKfPKGLIfVvEIdNEDVGKp
US-09-417- 306 lTtgeLSPSlFgNPtRKQlLlFvaseSEKlPIfEESkSKfPKGLIfVvEIdNEDVGKp
consensus -lFTRESAPlIfENRPKQlLlFAlSNDSEKlPIfEESkSKfPKGLIfVvEIdNEDVGKp

US-09-417- 330 VSEYFGISGNgPvLgTGTGNeDskRfVlaKEVtIdnIKaFgenFLEDKlKPFYKSdPvES
US-09-417- 347 VSEYFGISGNaPvLgTGTGNDgKkRfVlGGEvNadIKaFgddFLEDKlKPFYKSdPvES
US-09-417- 367 VadyFGlTgqetVlAYtGNeDARKfLDGEVslEaIKdFaeGfLEdKlLFPYKSdPvES
consensus VseYFGISGn-p-VlgTGTGNeD-kRfVlGGEvNad-ikAfgE-FLEDKlKPFYKSdPvES

US-09-417- 391 NDGDVkvVvGdNFDnAlVLDsKDVLLEIYAPWCGHCOALEPtyNKLAKHLRgIdSLVIAKM
US-09-417- 408 NDGDVkvIvGnNFDnAlVLDsKDVLLEIYAPWCGHCOALEPtyNKLAKHLRgIdSLVIAKM
US-09-417- 428 NDGDVkvIvGKNlDlIVfDECKDVLLEIYAPWCGHCOALEPtyNKLAKHLRgIdSLVIAKM
consensus NDGDVkvIvG-NFD-IVLDsKDVLLEIYAPWCGHCOALEPtyNKLAKHLR-IdSLVIAKM

US-09-417- 452 DGTtNEHPRAKSDGFPTlIfFPAGNKSFPdITVDTDRtVAlYKfIKKNaSlPFKlQKpvs
US-09-417- 469 DGTtNEHPRAKpDGFPTlIfFPAGNKSFPdITVDTDRtVAlYKfIKKNaSlPFKlQKp
US-09-417- 489 DGTtNEHPRAKSDGfPTlIfFPAGNKSFPdITfegERTVdVlYKfIKKNaSlPFKl
consensus DGTtNEHPRAKSDGFPTlIfFPAGNKSFPdITVdrtVAlYKfIKKNaSlPFKlQKpvs

US-09-417- 513 spKvSsEaKSGPAKESpKStLdVKDEL
US-09-417- 528 tStsdakYSSPAKES qSS DVKDEL
US-09-417- 545 krgesItESCrabgYKSSgtnSKDEL
consensus sp---s-----ssdakEs-kSS-LdVKDEL

Alignment score = 411.00
Scoring matrix:

4	94	289
5		213
8		